Gut Microbiota Dysbiosis Associated with Bile Acid Metabolism in Neonatal Cholestasis Disease

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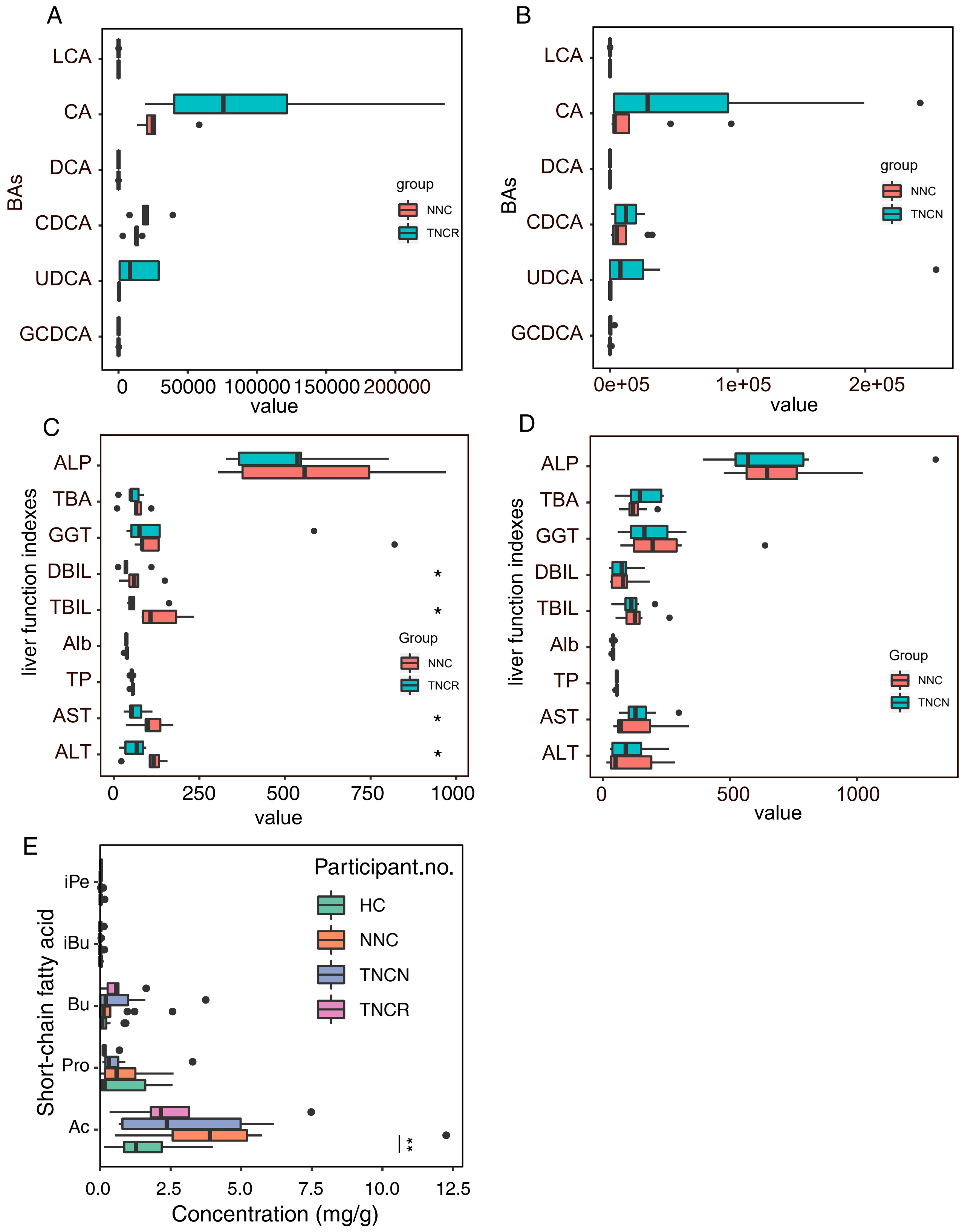
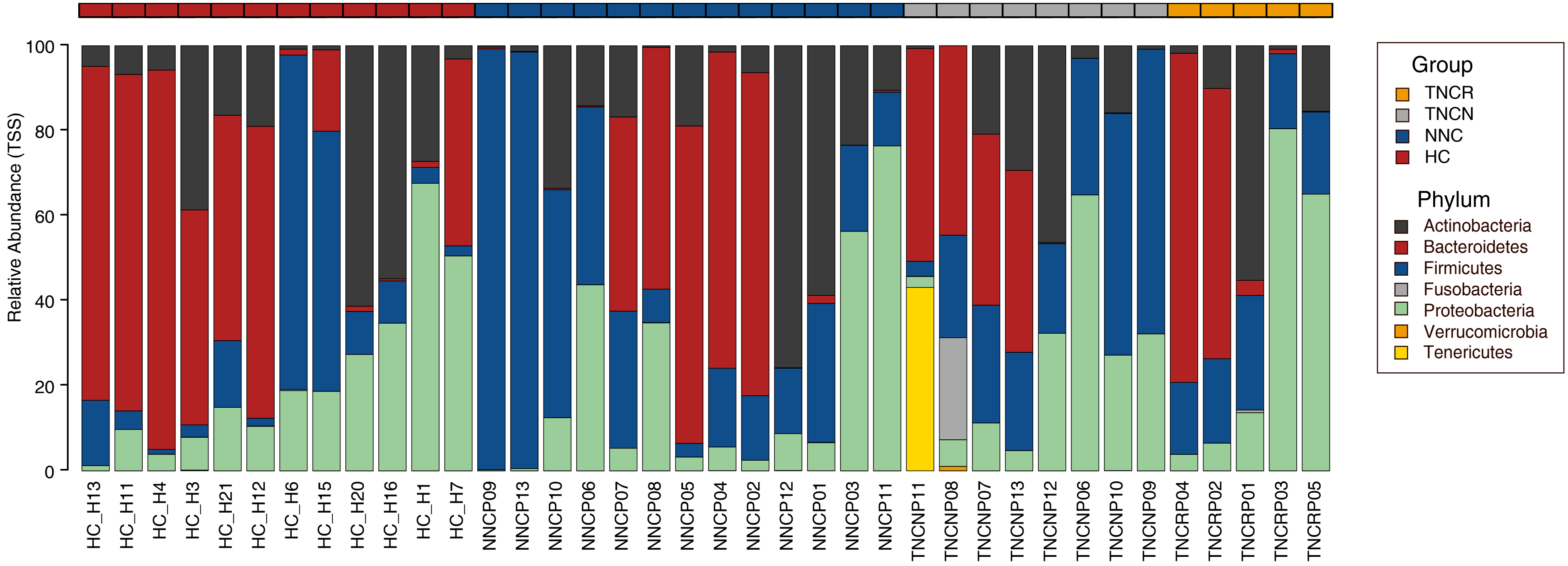
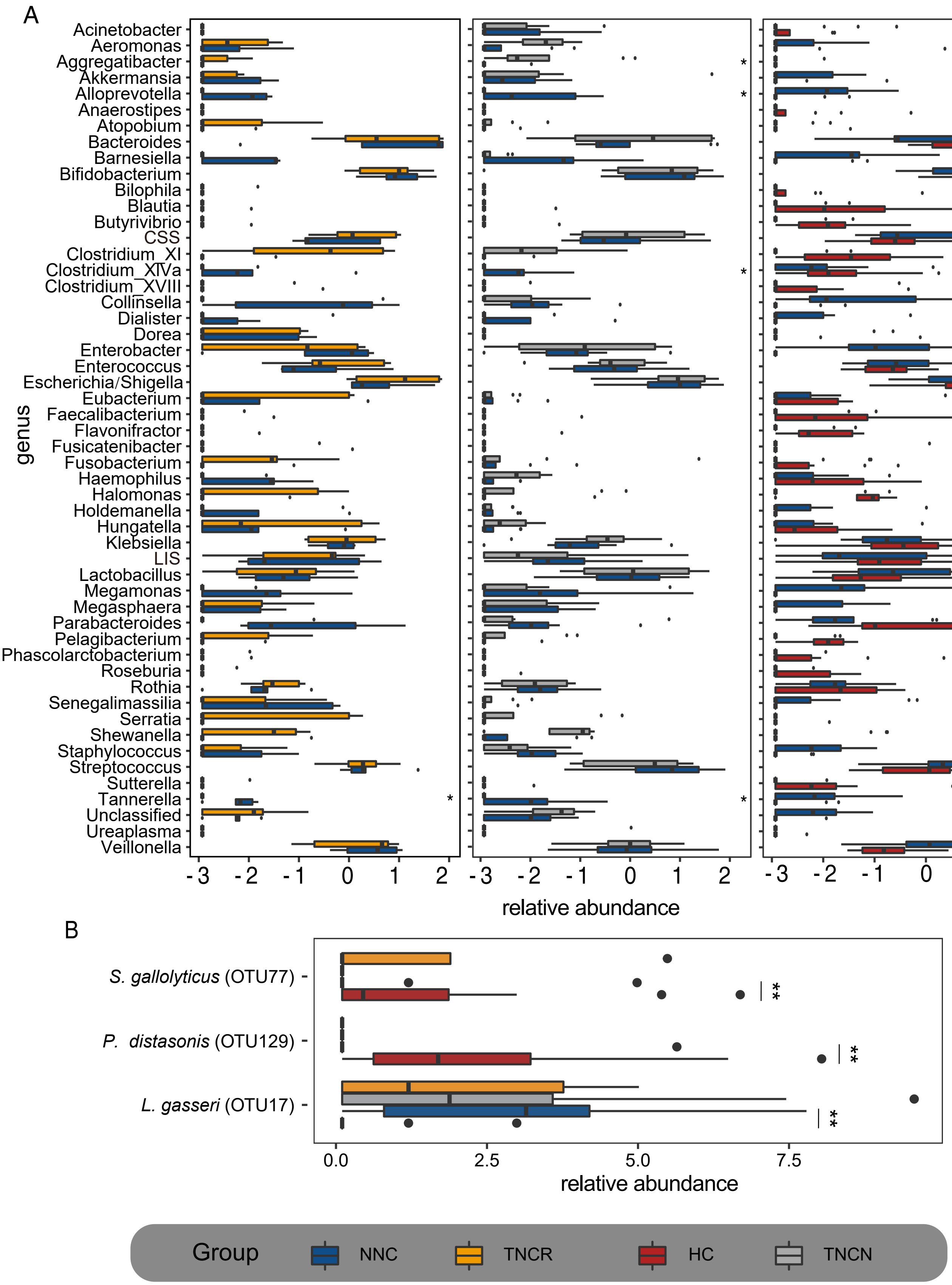


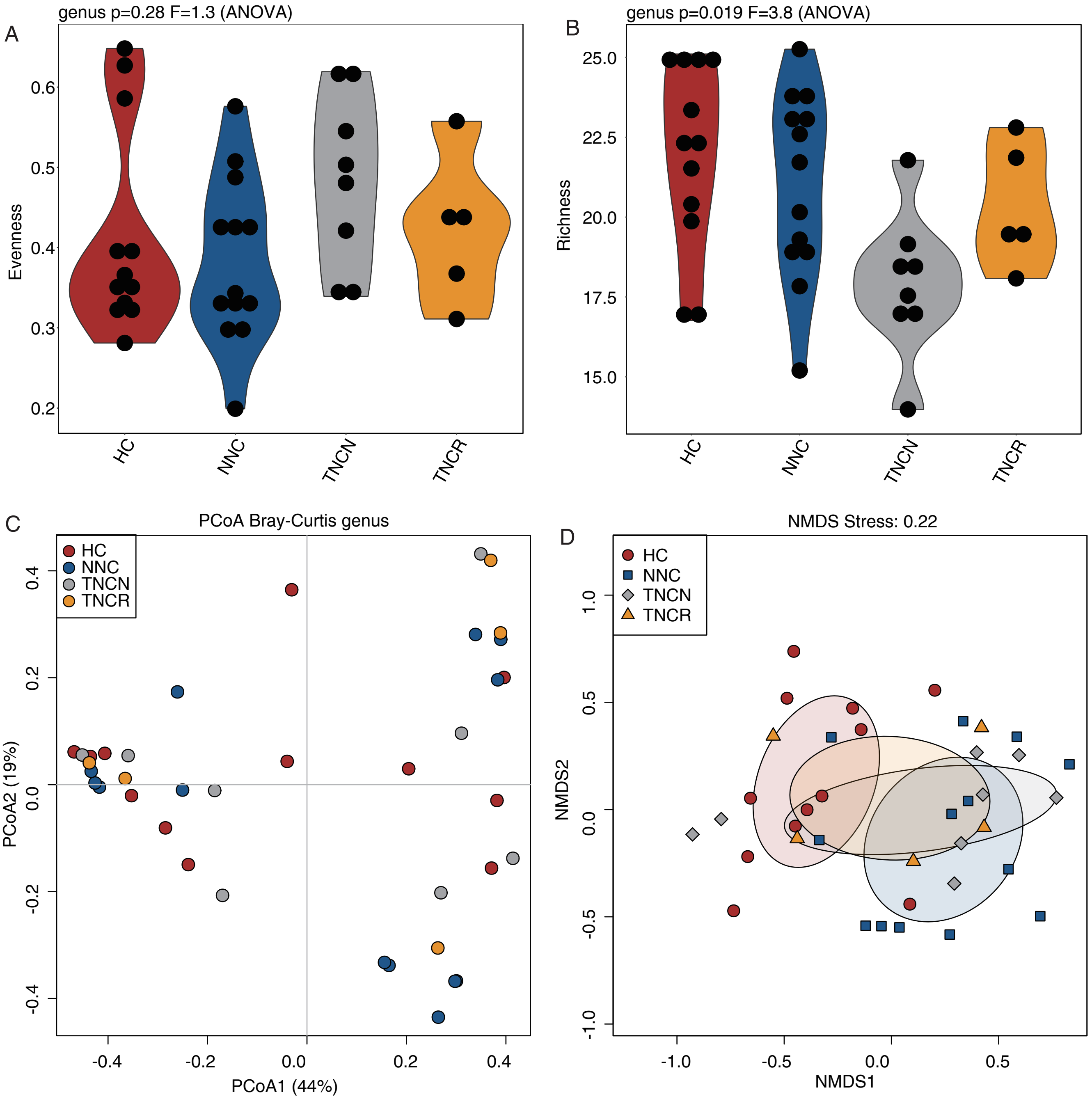
Additional file 1: BAs concentration (A and B) and liver function tests indexes(C and D) in stools results among NNC, TNCN, and TNCR groups, and SCFAs (E) results in four groups. Indexes unites of A, B, C and D were shown in additional file 6. *, $P<0.05$; **, $P<0.01$.



Additional file 2: microbiota distribution on phylum level. Yellow, darkred, gray, and blue represents TNCR, HC, TNCN, and NNC groups.



Additional file 3: microbiota difference analysis on genus level (A) and OTU level (B). *, *P*<0.05; **, *P*<0.01.



Additional file 4: part of microbiota alpha and beta analysis results. A and B were eveness and richness indexes of four groups. C and D shown microbiota beta diversity of four groups.